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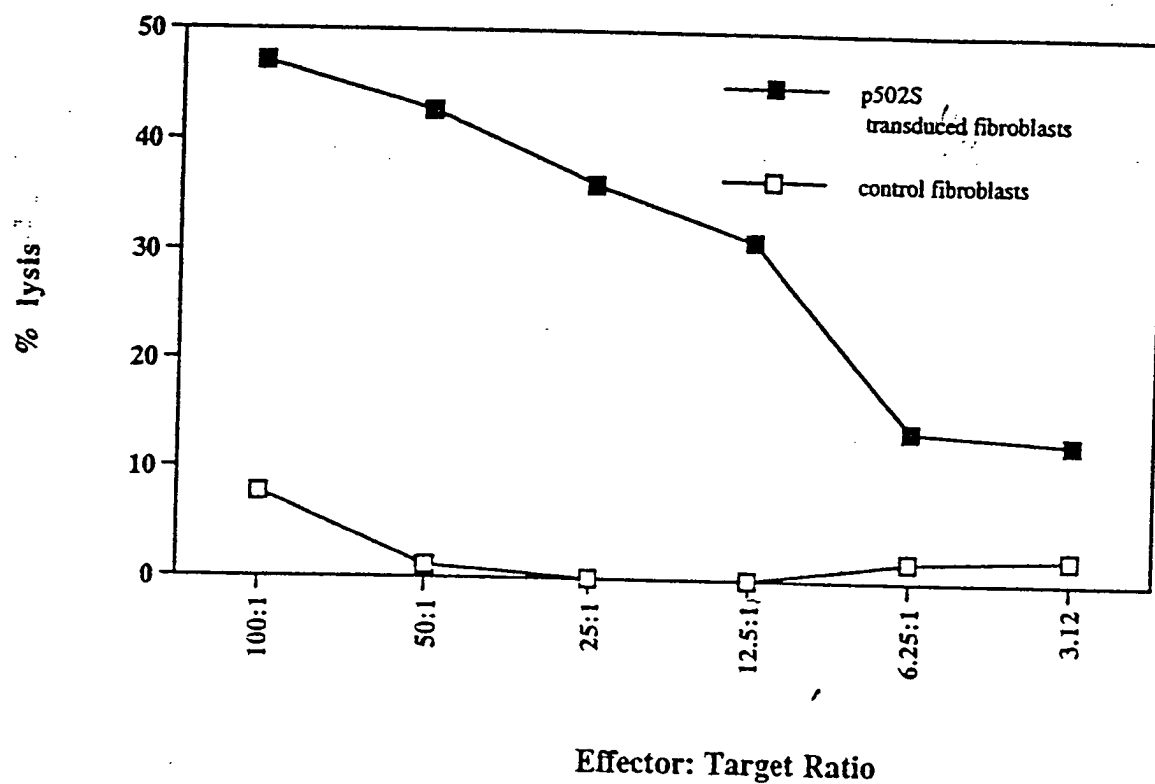
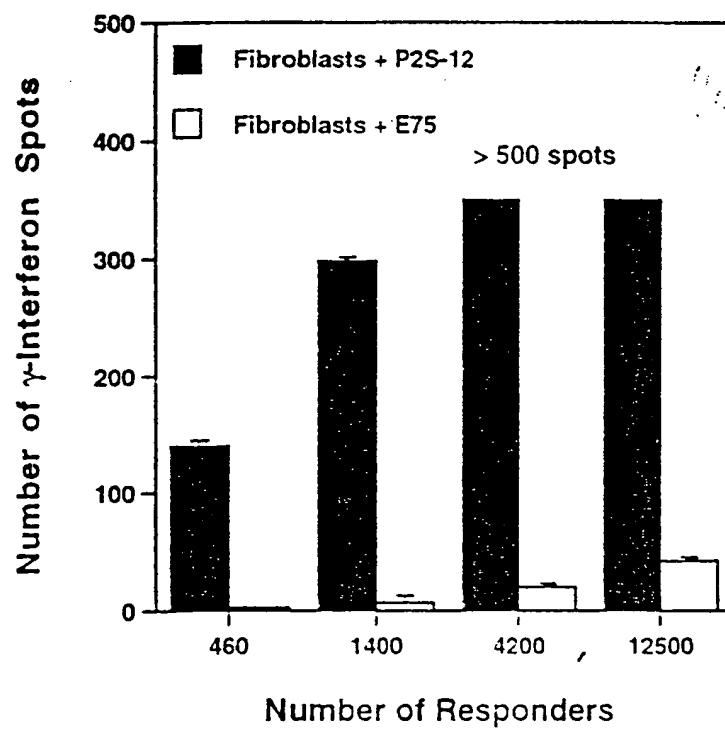
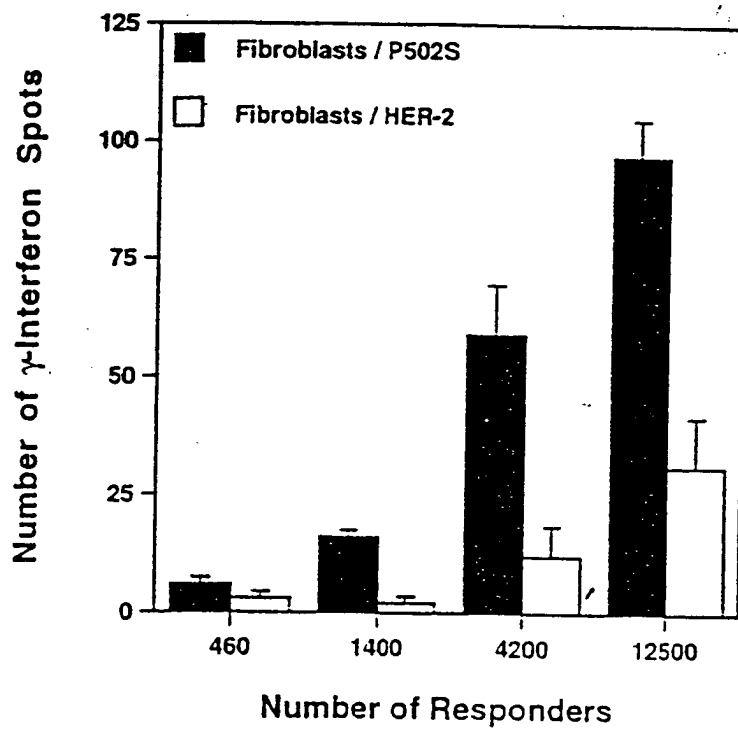


FIG. 1



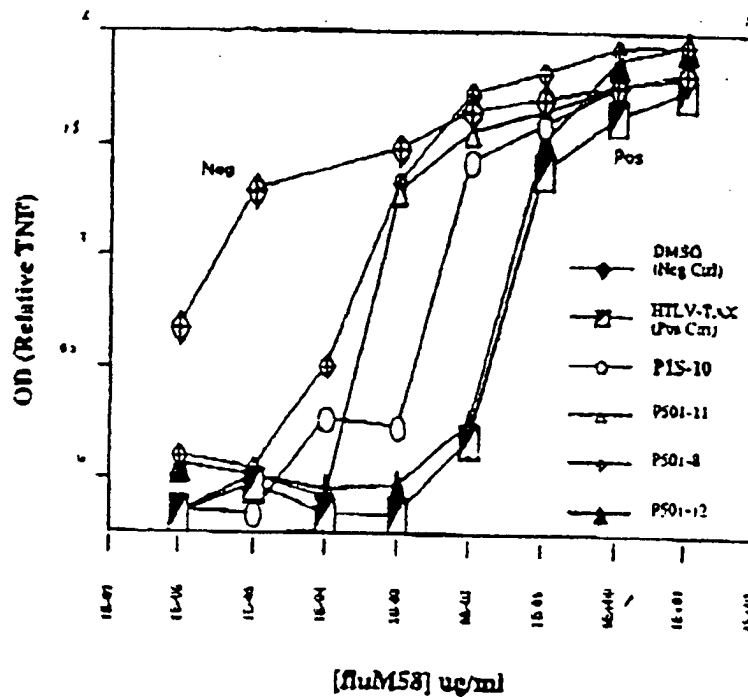
*FIG. 2A*

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*FIG. 2B*

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Figure

3

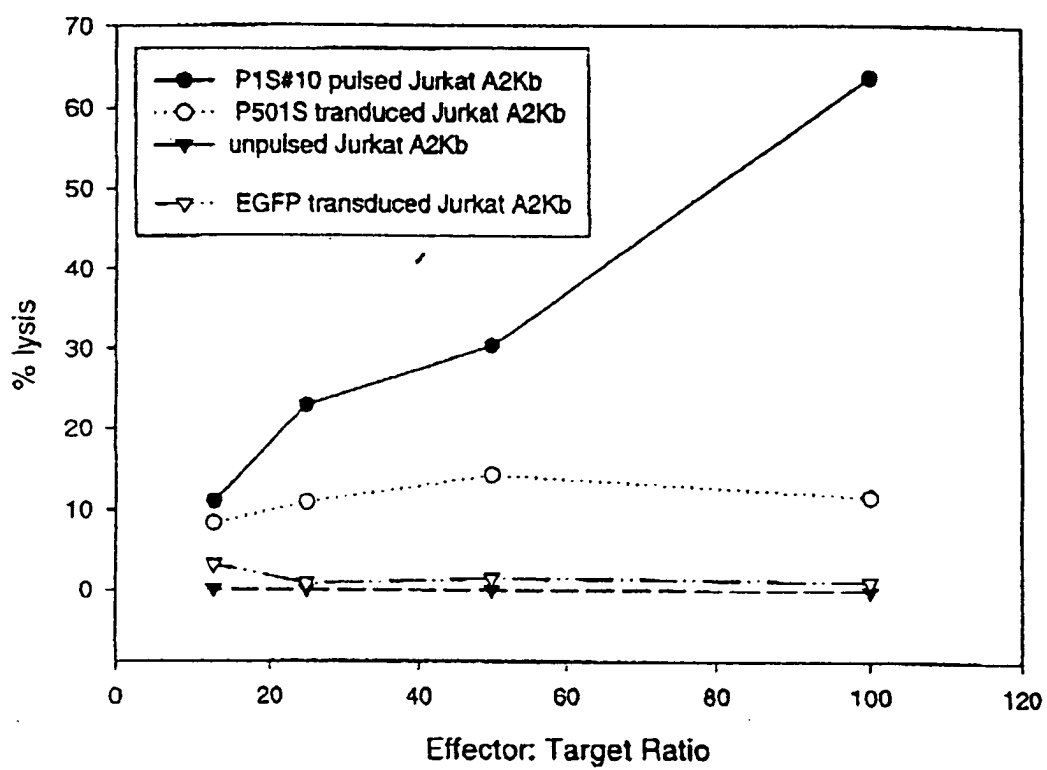


Figure 4

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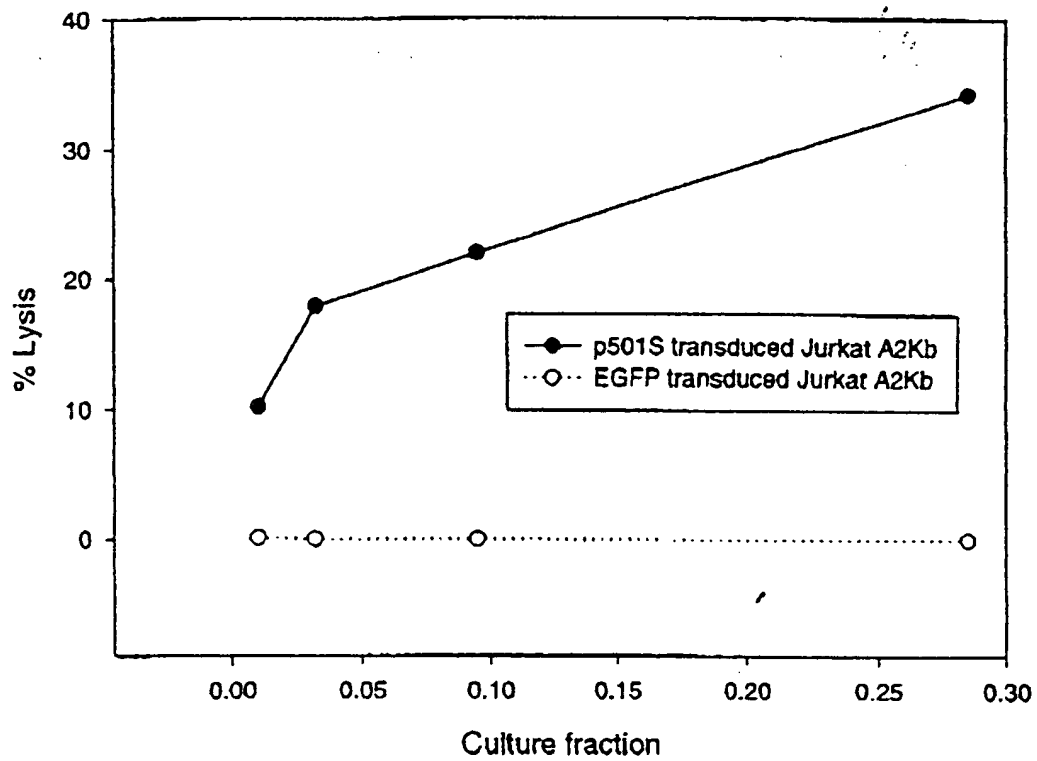


Figure 5

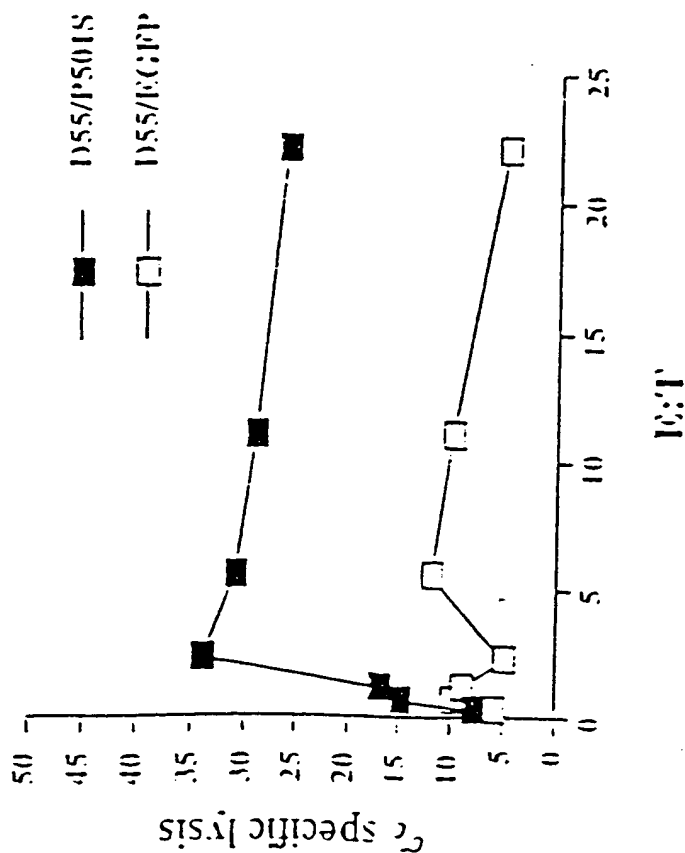


Fig. 6A

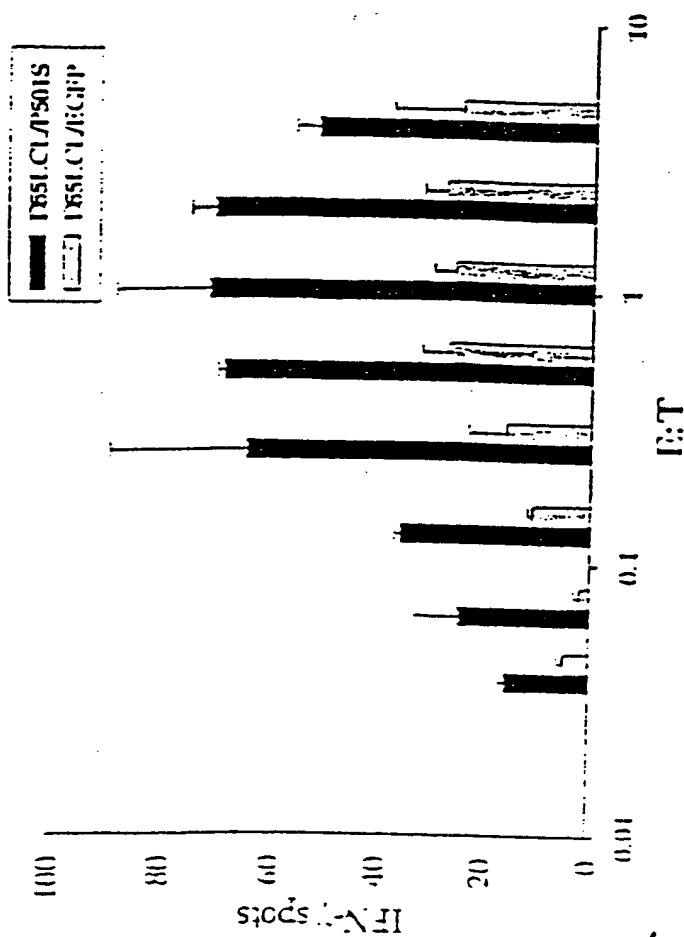
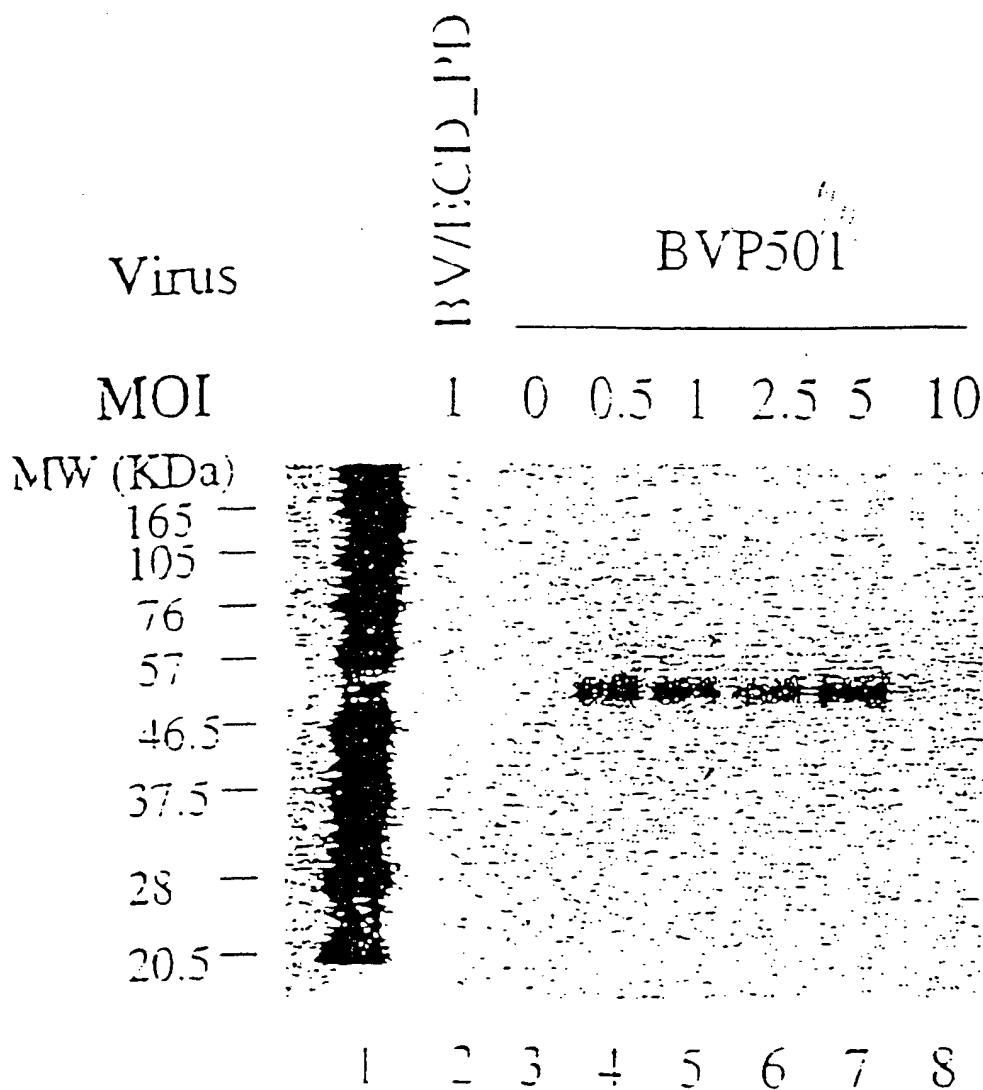


Fig. 6B

# Expression of P501S by the Baculovirus Expression System

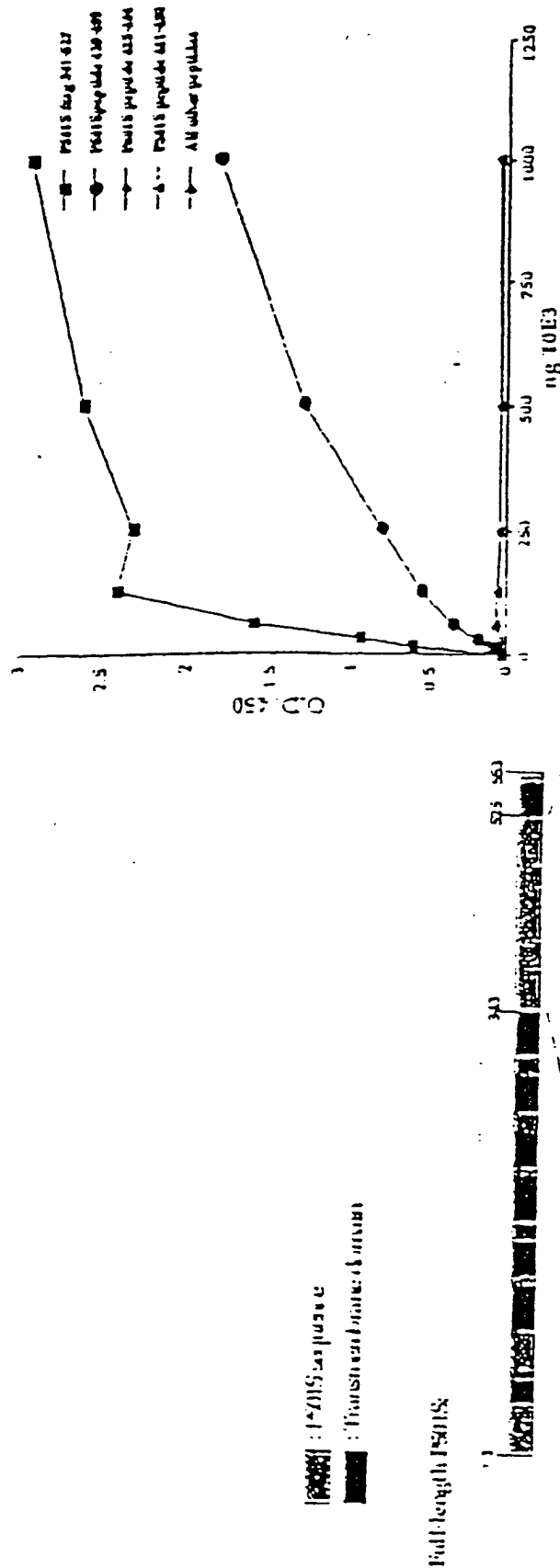


0.6 million high 5 cells in 6-well plate were infected with an unrelated control virus BV/ECD\_PD (lane 2), without virus (lane 3), or with recombinant baculovirus for P501 at different MOIs (lane 4 - 8). Cell lysates were run on SDS-PAGE under the reducing condition and analyzed by Western blot with a monoclonal antibody against P501S (P501S-IGEP-G4D3). Lane 1 is the biotinylated protein molecular weight marker (BioLabs).

Fig. 7



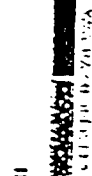
# Figure 8. Mapping of the epitope recognized by 10E3-G4-D3



Full length 10E3



10E3 fragment used for immunization:



10E3-G4-D3 (squares)

10E3-G4-D3 (circles)

10E3-G4-D3 (triangles)

10E3-G4-D3 (diamonds)

All other peptides

7

# Figure 1. Schematic of P501S with predicted transmembrane, cytoplasmic, and extracellular regions

AVQRLAVSRLLRIK AQLIAYNLLTGLFVCLAACTVVPPLLEEVGVFEKEMTNVIGIGPYVLGLYCVPLIGSAS  
 DHWRGRYGRRRP FIWALSGLHLSLEFLPRAGWL AGLCPDPRPLE LALLHGVGLLDLFCGQVCFPL  
 FALSDFRDPDHCRQ AYSVYAFHLSLGGCTGYLTPAI DWIVSALAPVLCQRE  
 CLTGLHLLFLTCYAAATLLY AFEAAIGPTEPAKGLSAPVSPICCTGRARAFRNIGAILPRI  
 HQLCCRAPIRTHH LPYAEFLCSWMANLITFYTOP YGEGLYQGVPRAPPGTLEARRHIYDEGYR  
 MGSGLFLFOCAISLYFSLVM DRLYQRECTRAVYLAS YAAFTPYAAGATCLSHSYAVVTA SAA  
 LTGETFSALOILFYTLASLY HREKQVFLPKYRGDTGGASSEDLSMTSELPQPKPGAPFPNGHIVGAGGSGL  
 LPPPPALCGASACDVSVRVVVGEPTEARVVVGRG ICLDILAILPSAFELLSQVAPSLF MGSIVQLSQS  
 VTAYMVSAAGLGLYALYFAT QVVFDKSDIAKYSY

Underlined sequence: Predicted transmembrane domain; Bold sequence: Predicted extracellular domain;  
 Italic sequence: Predicted intracellular domain. Sequence in bold/underlined: used to generate polyclonal rabbit serum

Localization of domains predicted using IMMTOPI (G.E. Tusnady and L. Simon (1998) Principles  
 Governing Amino Acid Composition of Integral Membrane Proteins: Applications to topology Prediction. J. Mol Biol. 283,  
 489-506.

# Genomic Map of (5) Corlxa Candidate Genes

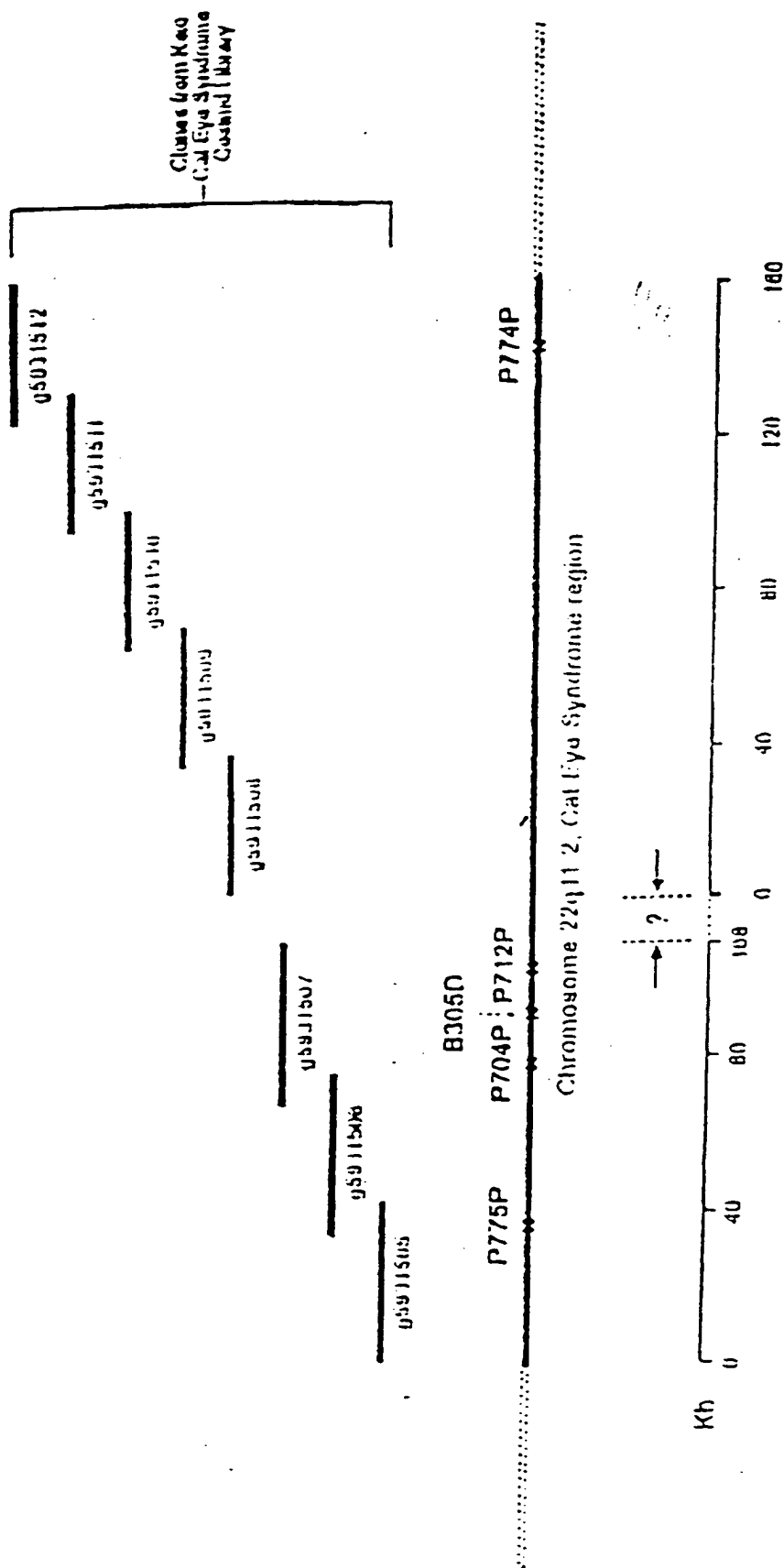


Fig. 10

**FIGURE 4. Elisa assay of rabbit polyclonal antibody specificity**

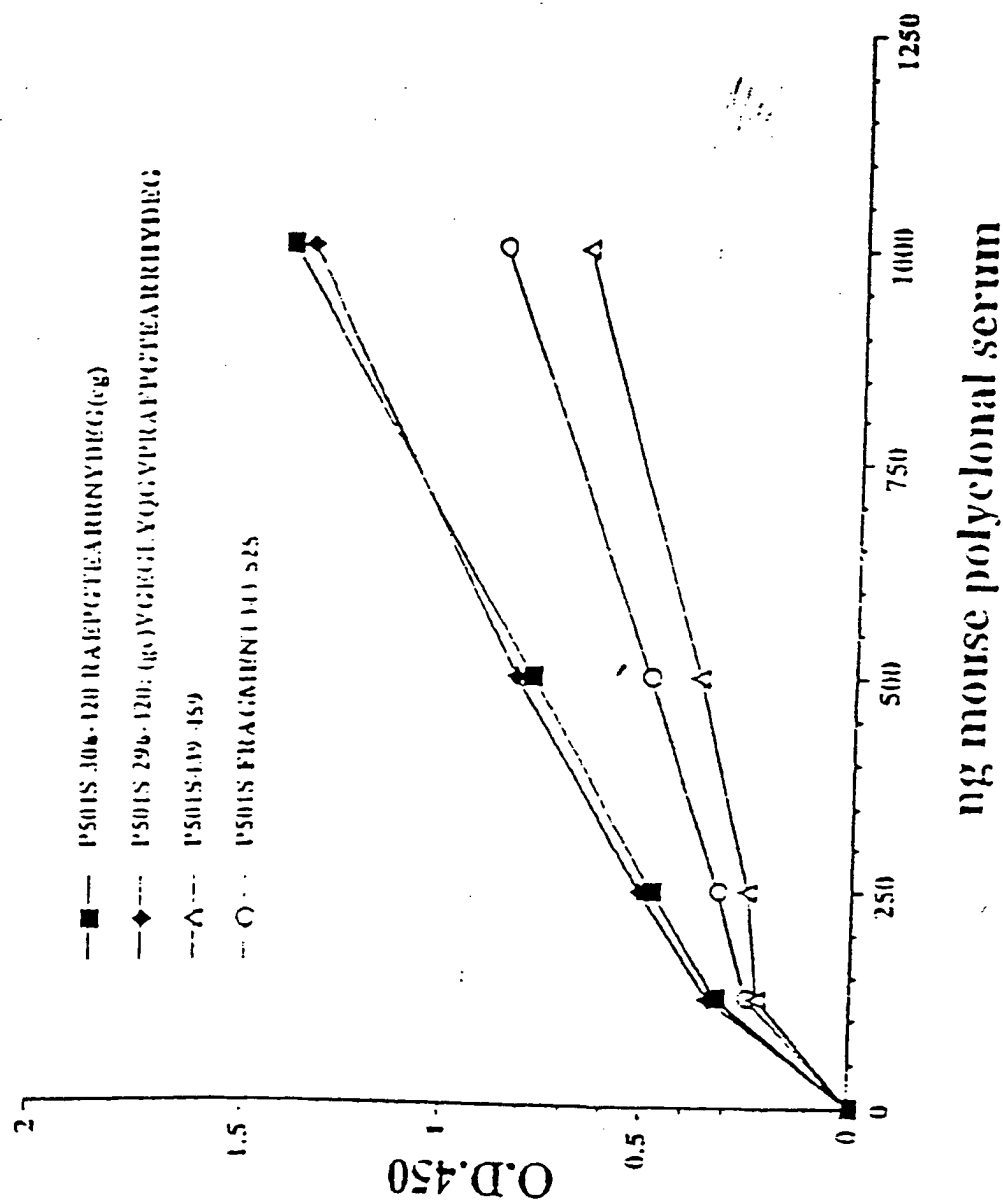


Fig. 11

10	20	30	40	50	60	70
GTCACCTAGGAAAAGGTGTCCTTTTCGGGCAGCCGGGCTCAGCATGAGGAACAGAAGGAATGACACTCTGG 70						
ACAGCACCCGGACCCTGTACTCCAGCGCGTCTCGGAGCACAGACTTGTCTTACACTGAAAGCGACTTGGT 140						
GAATTTTATTCAAGCAAATTTTAAAGAAACGAGAATGTGTCTTCTTTACCAAAGATTCCAAGGCCACGGAG 210						
AATGTGTGCAAGTGTGGCTATGCCAGAGCCAGCAGATGGAAGGCACCCAGATCAACCAAAGTGAGAAAT 280						
GGAACTACAAGAAACACACCAAGGAATTTCTTACCGAGCCCTTTGGGGATATTTCAGTTTGAGACACTGGG 350						
360	370	380	390	400	410	420
GAAGAAAGGGAAGTATATACGTCTGTCTTGCAGACAGGACGGGAAATCCTTTACGAGCTGCTGACCCAG 420						
CACTGGCACCCTGAAAACAACCAACCTGGTCATTTCTGTGACCGGGGGCGCCAAGAACTTCGCCCTGAAGC 490						
CGCGCATGCGCAAGATCTTCAGCCGGCTCATCTACATCGCGCAGTCCAAAGGTGCTTGGATTCTCACGGG 560						
AGGCACCCATTATGGCCTGACGAAGTACATCGGGGAGGTGGTGAGAGATAACACCATCAGCAGGAGTTCA 630						
GAGGAGAATATTGTGGCCATTGGCATAGCAGCTTGGGGCATGGTCTCCAACCGGACACCCCTCATCAGGA 700						
710	720	730	740	750	760	770
ATTGGCATGCTGAGGGCTATTTTTTAGCCCAAGTACCTTATGGATGACCTCACAAGGGATCCACTGTATAT 770						
CCTGGACAACAACACACACATTTGCTGCTCGTGGACAAATGGCTGTGATGGACATCCCACTGTGGAAGCA 840						
AAGCTCCGGAAATCAGCTAGAGAAGCATATCTCTGAGCGCACTATTCAAGATTCCAACTATGGTGGCAAGA 910						
TCCCCATTGTGTGTTTGGCCAAAGGAGGTGGAAAAGAGACTTGAAGGCCATCAATACCTCCATCAAAAA 980						
TAAAAATTCCTTGTTGGTGGTGGAAAGGCTCGGGCGGATCGCTGATGTGATCGCTAGCCTGGTGGAGGTG 1050						
1060	1070	1080	1090	1100	1110	1120
GAGGATGCCCGACATCTTTCTGCGGTCAAGGAGAAAGCTGGTGGGCTTTTTTACCCCGCACGGTGTCTCGGC 1120						
TGTCTGAGGAGGAGACTGAGAGTTGGATCAAATGGCTCAAAGAAATTTCTGCAATGTTCTCACCTATTAAC 1190						
AGTTATTAAAAATGGAAGAAAGCTGGGGATGAAATTTGTAGCAATGGCATCTCTACGCTCTATACAAAGCC 1260						
TTCAGCACCAAGTGAGCAAGACAAAGGATAAOTGGAATGGGCAGCTGAAGCTTCTGCTGGAGTGGAAACAGC 1330						
TGGACTTAGCCCAATGATGAGATTTTCACCAATGACCGCGGATGGGAGTCTGCTGACCTTCAAGAAATCAT 1400						
1410	1420	1430	1440	1450	1460	1470
GTTTACGGCTCTCATAAAGGACAGACCCAAGTTTGTCCGCTCTTTCTGGAGAATGGCTTGAACCTACGG 1470						
AAGTTTCTCACCCATGATGTCCTCACTGAACCTCTCTCCAAGCACTTCAGCACGCTTGTGTACCGGAATC 1540						
TGCAGATCGCCAAGAATTCTTATAATGATGCCCTCTCTACGTTTGTCTGGAACTGGTTGCGAATTTCCG 1610						
AAGAGGCTTCGGGAAGGAAGACAGAAATGGCCGGGATGAGATGGACATAGAATCCACGACGTGTCTCT 1680						
ATTACTCGGCACCCCTGCAAGCTCTCTTCATCTGGGCCATTCTTCAGAAAGGAAGGAACCTCCAAAG 1750						
1760	1770	1780	1790	1800	1810	1820
TCATTTGGGAGCAGACACAGGGGCTGCACTCTGGCAGCCCTGGGAGCCAGCAAGCTTCTGAAGACTCTGGC 1820						
CAAAGTGAAGAAGACATCAATGCTGCTGGGGAGTTCGAGGAGCTGGCTAATGAGTACGAGACCCGGGCT 1890						
GTTGAGCTGTTCACTGAGTGTACAGCAGCGATGAAGACTTGGCAGAACAGCTGCTGGTCTATTCTGTG 1960						
AAGCTTGGGGTGGAAAGCAACTGTCTGGAGCTGGCGGTGGAGGGCAGAGACCAAGCATTTACCGGCCAGCC 2030						
TGGGGTCCAGAAATTTCTTTCTAAGCAATGGTATGGAGAGATTTCCCGAGACACCAAGAACTGGAAGATT 2100						

Fig. 12A (i)

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2110	2120	2130	2140	2150	2160	2170
<p>TCCTGTGTCTGTTTATTATACCCTTGGTGGGCTGTGGCTTTGTATCATTTAGGAAGAAACCTGTCGACA 2170</p> <p>AGCACAAGAAGCTGCTTTGGTACTATGTGGGCTCTTCACCTCCCCCTTCGTGGTCTTCTCCTGGAATGT 2240</p> <p>GGTCTTCTACATCGCCTTCCCTCCTGCTGTTGGCTACGTGCTGCTCATGGATTTCCATTGGTGCCACAC 2310</p> <p>CCCCCGAGCTGCTCCTGTACTCCCTGGCTTTGTCTCTTCTGTGATGAAGTCAGACAGTGGTACGTA 2380</p> <p>ATGGGGTGAATTATTTTACTGACCTGTGGAATGTGATGGACACGCTGGGGCTTTTTTACTTCATAGCAGG 2450</p>						
2460	2470	2480	2490	2500	2510	2520
<p>AATTGTATTTGGGCTCCACTCTTCTAATAAAAGCTCTTTGTATTCTGGACGAGTCATTTTCTGTCTGGAC 2520</p> <p>TACATTATTTTCACTCTAAGATTGATCCACATTTTACTGTAAGCAGAAACTTAGGACCCAAGATTATAA 2590</p> <p>TGCTGCAGAGGAI GCTGATCGATGTGTCTTCTTCTCTGTTCTCTTTGCGGTGTGGATGGTGGCCTTTGG 2660</p> <p>CGTGGCCAGGCAAGGGATCCTTAGGCAGAAATGAGCAGCGCTGGAGGTGGATATTCGGTTGGTTCATCTAC 2730</p> <p>GAGCCCTACCTGGCCATGTTCCGCCAGGTGCCAGTGACGTGGATGGTACCACGATGACTTTGCCCACT 2800</p>						
2810	2820	2830	2840	2850	2860	2870
<p>GCACCTTCACTGGGAATGAGTCCAAGCCACTGTGTGTGGAGCTGGATGAGCACAACCTGCCCGGGTTCCC 2870</p> <p>CGAGTGGATCACCATCCCCCTGGTGTGCATCTACATGTTATCCACCAACATCCTGCTGGTCAACCTGCTG 2940</p> <p>GTCGCCATGTTTGGCTACACGGTGGGCACCGTCCAGGAGAAACAATGACCAGGTCTGGAAGTCCAGAGGT 3010</p> <p>ACTTCTTGGTGCAGGAGTACTGCAGCGCGCTCAATATCCCCCTTCCCCCTTCACTGCTTGGCTTACTTCTA 3080</p> <p>CATGGTGGTGAAGAAGTGTCTCAAGTGTGTGTGAAGGAGAAAAACATGGAGTCTTCTGTCTGTCTGTTTC 3150</p>						
3160	3170	3180	3190	3200	3210	3220
<p>AAAAATGAAGACAATGAGACTCTGGCATGGGAGGGTGTGATGAAGGAAAACCTACCTTGTCAAGATCAACA 3220</p> <p>CAAAAACCAACGACACCTCAGAGGAAATGAGGCACTGATTTAGACAACTGGATACAAAGCTTAATGATCT 3290</p> <p>CAAGGGTCTCTGAAAAGAGATTGGTAAATAAAATCAATAAAACTGTATGAAACTCTAATGGAGAAAAATC 3360</p> <p>TAATTATAGCAAGATCATATTAAGGAATGCTGATGAACAATTTTGGTATCGACTACTAAAAGAGAGATT 3430</p> <p>TCAGACCCCTGGGTACATGGTGGATGATTTTAAATCACCTAGTGTGCTGAGACCTTGAGAATAAAGTGT 3500</p>						
3510	3520	3530	3540	3550	3560	3570
<p>GTGATTGGTTCATACTTGAAGACGGATATAAAGGAAGAAATATTTCTTTTATGTGTTTCTCCAGAATGGT 3570</p> <p>GGCTGTTTCTCTCTGTGTCTCAATGGCTGGGACTGGAGGTTGATAGTTTAAGTGTGTTCTTACCGCTCC 3640</p> <p>TTTTTCTTTTAACTCTTATTTTGGTGAACACATATATAGGAGAACATCTATCCTATGAATAAGAACCTGG 3710</p> <p>TCATGCTTTACTCCTGTATTGTTATTTTGTTCATTTCCAAATGATTCTCTACTTTTCCCTTTTGTATT 3780</p> <p>ATGTGACTAATTAGTTGGCATATTGTTAAAGTCTCTCAATTAGGCCAGATTCTAAAACATGCTGCAGC 3850</p>						
3860	3870	3880	3890	3900	3910	3920
<p>AAGAGGACCCCGCTCTCTTCCAGGAAAAAGTGTCTTCATTTCTCAGGATGCTTCTTACCTGTGAGAGGAGGT 3920</p> <p>GACAAGGCACTCTCTTGTCTCTTGGACTCAGCAGGCTCTATTGAAGGAACCCCCCATTCCTAAATA 3990</p> <p>TGTGAAAAGTCCCCCAAAATGCAACCTTGAAAGGCACTACTGACTTTGTTCTTATTGGATACTCCTTTA 4060</p> <p>TTTATTATTTTCCATTAAAAAATAGGTGGCTATTATAGAAAATTTAGACCATACAGAGATGTAGAAA 4130</p> <p>GAACATAAATTTGCCCCATTACCTTAAGGTAATCACTGCTAACAATTTCTGGATGGTTTTTCAAGTCTAT 4200</p>						
4210	4220	4230	4240	4250	4260	4270
<p>TTTTTTCTATGATGTCTCAATTCTCTTTCAAAATTTACAGAAATGTTATCATACTACATATATACTTT 4270</p> <p>TTATGTAAGCTTTTTCACTTAGTATTTTATCAAAATATGTTTATTATATTCATAGCCTTCTTAACATT 4340</p> <p>ATATCAATAATTGCAATAAGGCAACCTCTAGCGATTACATAAATTTGCTCATTTGAAGGCTATCTCCAG 4410</p> <p>TTGATCATTTGGGATGAGCACTCTTGTGCAATGAATCCTATTGCTGTAATTGGGAAAATTTTCCAAGGTTAG 4480</p> <p>ATTCCAATAAATATCTATTTATTATTAAATATTAAATATCGATTATTATTAAACCATTATTAAGGCT 4550</p>						

Fig. 12A(2)

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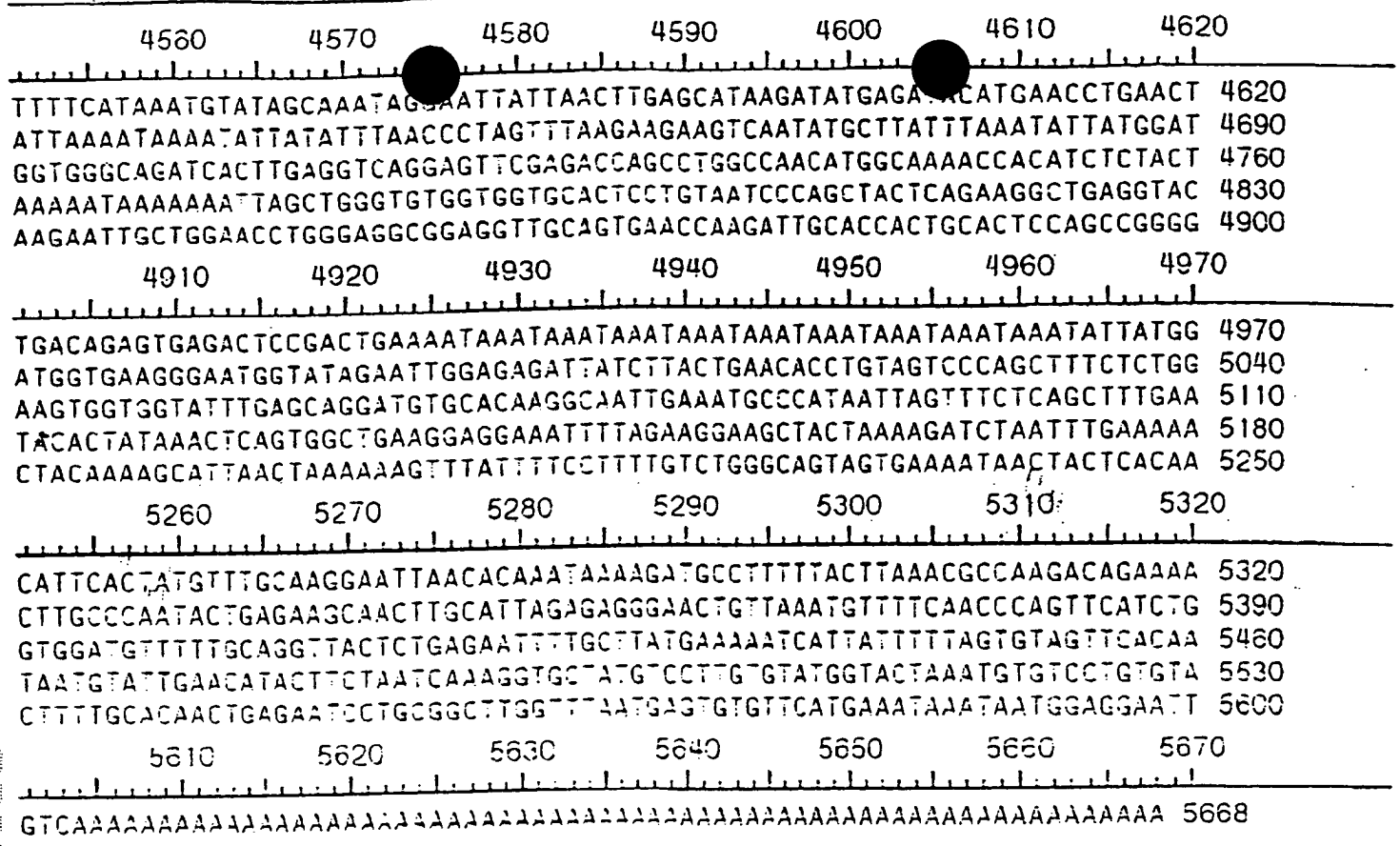


Fig. 12A(3)

10 20 30 40 50 60 70  
 MRNRRNDTLOSTRTRYSSASRSTOLSYSESOLVNFIOANFKKRECVFFTKDSKATENVCKCGYAQSOHME 70  
 GTQINQSEKWNYYKKHTKEFPTDAFGDIQFETLGKKGKYIRLSCDTDAEILYELLTQHWHLKTPNLVISVT 140  
 GGAKNFALKPRMRKIFSRLLYIAQSKGAWILTGGTHYGLTKYIGEYVRONTISRSEENIVAIGIAAWGM 210  
 VSNRDTLIRNCDAEGYFLAQYLMDDFTRDPLYLQNNHHTHLLVDNGCHGHPTVEAKLRNQLKHSERT 280  
 IQDSNYGGKIPYVCFAGGGGKETLKAINTSIKKNPCYVVEGSGRIAQVIASLVEVEDAPTSSAVKEKLV 350  
 360 370 380 390 400 410 420  
 RFLPRTVSRLSEEETESWIKWLKEILECSHLLTVIKMEEAGDEIVSNAISYALYKAFSTSEQDKDNWNGQ 420  
 LKLLLEWNQDLANDEIFTNDRRWESADLOEVMFTALIKDRPKFYRLFLENGLNLRKFLTHOVLTELF 490  
 HFSTLVYRNLGIAKNSYNDAALLTFVWKLVANFRRGFRKEDRNGROEMOIELHGVSPITRHPLQALFIWA 560  
 LQNKKELSKVIWEGTRGCTLAALGASKLLKTLAKYKNDINAAGESEELANEYETRAVELFTECYSSOEDL 630  
 AEQLLVYSCEAWGGSNCLELAVEATDQHFTAQPGVQNFLSKQWYGEISRDTKNWKILCLFIIPLVGCGF 700  
 710 720 730 740 750 760 770  
 VSFRKKPVQKHKKLLWYYVAFFTSPFVVFVSWNVVFYIAFLLLFAYVLLMDFHSVPHPPPELVLYSLVFVLF 770  
 CDEYRQWYVNGVNYFTDLWNVMOTLGLFYFIAGIVFRHSSNKSSLYSGRVIFCLDYIFTLRLIHIFTV 840  
 SRNLGPKIIMLQRMLOVFFFLFLFAYWMVAFGVARGGILRONEGRWRWIFRSVIYEPYLA MFGQVPSDV 910  
 DGTTYDFAHCTFTGNEKPLCVELDEHNLPRFPEWITIPLVCIYMLSTNILLVNLVAMFGYTVGTVGEN 980  
 NQGVWKFGRYFLVQEYCSRLNIPFPFIVFAYFYMVVKKCFKCCCKEKNMESSVCCFKNEDNETLAWEGVM 1050  
 1060 1070 1080 1090 1100 1110 1120  
 KENYLVKINTKANOTSEEMRHRFRQDITKLNOLKGLKEIANKIK. 1096

Fig. 12B

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